



H5-2

Phe	Phe	Thr	Ser	Phe	Tyr	Trp	Ser	Phe	Ile	Thr	Met	Thr	Thr	Val	Gly	Phe	Gly	Asp	Leu	180
TTC	TTC	ACT	TCA	TTC	TAC	TGG	TCC	TTC	ATT	ACA	ATG	ACT	ACT	GTC	GGG	TTT	GGC	GAC	TTG	540
Met	Pro	Arg	Arg	Asp	Gly	Tyr	Met	Tyr	Ile	Ile	Leu	Leu	Tyr	Ile	Ile	Leu	Gly	Lys	Phe	200
ATG	CCC	AGA	AGG	GAC	GGA	TAC	ATG	TAT	ATC	ATA	TTG	CTC	TAT	ATC	ATT	TTA	GGT	AAA	TTT	600
Ser	Met	Lys	Lys	Lys	Gln	Lys	Phe	Lys	Ile	Phe	Leu	Gly	Leu	Ala	Ile	Thr	Thr	Met	Cys	220
TCA	ATG	AAA	AAA	AAA	CAA	AAA	TTC	AAA	ATA	TTT	TTA	GGT	CTT	GCA	ATA	ACT	ACA	ATG	TGC	660
Ile	Asp	Leu	Val	Gly	Val	Gln	Tyr	Ile	Arg	Lys	Ile	His	Tyr	Phe	Gly	Arg	Lys	Ile	Gln	240
ATT	GAT	TTG	GTA	GGA	GTA	CAG	TAT	ATT	CGA	AAG	ATT	CAT	TAT	TTC	GGA	AGA	AAA	ATT	CAA	720
Asp	Ala	Arg	Ser	Ala	Leu	Ala	Val	Val	Gly	Lys	Val	Val	Val	Leu	Val	Ser	Glu	Leu	Tyr	260
GAC	GCT	AGA	TCT	GCA	TTG	GCG	GTT	GTA	GGA	GGA	AAG	GTA	GTC	CTT	GTA	TCA	GAA	CTC	TAC	780
Ala	Asn	Leu	Met	Gln	Lys	Arg	Ala	Arg	Asn	Met	Ser	Arg	Glu	Ala	Phe	Ile	Val	Glu	Asn	280
GCA	AAT	TTA	ATG	CAA	AAG	CGA	GCT	CGT	AAC	ATG	TCC	GAA	GCT	TTT	ATA	GTG	GAG	AAT	840	
Leu	Tyr	Val	Ser	Lys	His	Ile	Ile	Pro	Phe	Ile	Pro	Thr	Asp	Ile	Arg	Cys	Ile	Arg	Tyr	300
CTC	TAT	GTT	TCC	AAA	CAC	ATC	ATA	CCA	TTT	ATA	CCA	ACT	GAT	ATC	CGA	TGT	ATT	CGA	TAT	900
Ile	Asp	Gln	Thr	Ala	Asp	Ala	Ala	Thr	Ile	Ser	Thr	Ser	Ser	Ser	Ala	Ile	Asp	Met	Gln	320
ATT	GAT	CAA	ACT	GCC	GAT	GCT	ACC	GCT	ACC	ATT	TCC	ACG	TCA	TCG	TCT	GCA	ATT	GAT	ATG	960
Ser	Cys	Arg	Phe	Cys	His	Ser	Arg	Tyr	Ser	Leu	Asn	Arg	Ala	Phe	Lys					336
AGT	TGT	AGA	TTT	TGT	CAT	TCA	AGA	TAT	TCT	CTC	AAT	CGT	GCA	TTC	AAA	TAG				1011

(SEQ ID NO:4)  
(SEQ ID NO:3)

FIG. 3B



(SEQ ID NO: 7) mIRK  
 (SEQ ID NO: 8) hROMK1  
 (SEQ ID NO: 9) rGIRK1  
 (SEQ ID NO: 10) Dm H5-1  
 (SEQ ID NO: 11) Shak  
 (SEQ ID NO: 12) Shal  
 (SEQ ID NO: 13) Shab  
 (SEQ ID NO: 14) Shaw  
 (SEQ ID NO: 15) Eag  
 (SEQ ID NO: 16) S10  
 (SEQ ID NO: 17) Dm H5-2

(SEQ ID NO: 18) Dm H5-1  
 (SEQ ID NO: 19) Ce 5-1  
 (SEQ ID NO: 20) Dm H5-2  
 (SEQ ID NO: 21) Ce H5-2

AFLFSIETQTTIGYGFRVTECP  
 AFLFSLETQVTIGYGFRCVTEQCA  
 AFLFFIETEATIGYGYRYITDHCP  
 . . . . .  
 AFFFAFTVCSTVGYGNISPTTFAG  
 . . . . .  
 AFWWAVVTMTTVGYGDMTPVGFWG  
 AFWYTIVTMTTLGYGDMVPETIAG  
 AFWWAGITMTTVGYGDIPTTALG  
 GLWWALVTMTTVGYGDMAPKTYIG  
 ALYFTMTTCMTSVGFGNVAAETDNE  
 CVYFLIVTMSTVGYGDVYCETVLG  
 . . . . .  
 SLYTSYVTTTTIGFGDYVPTFGAN

{G,A,S,T}, {D,E}  
 {N,Q}, {K,R,H}  
 {F,Y,W} = {I,L,M,V}

AFFFAFTVCSTVGYGNISPTTFAG  
 SIFFAVTVVTTIGYGNPVPVNTG  
 SLYTSYVTTTTIGFGDYVPTFGAN  
 SFYWSFITMTTVGFGDLMPRRDGY

FIG. 5A

Tyr His Tyr His His Gln Lys Gly Met Glu Ile Arg Glu Lys Ala Glu Thr Asp Arg Pro Ser Pro Ser Ile Leu  
 TAC CAC TAT CAC CAT CAA AAA GGA ATG GAA ATT CGC GAA AAG GCG GAA ACC GAC AGA CCG TCT CCA TCC ATT CTT 230 240 250  
 750  
 Trp Thr Thr Phe Thr Asn Cys Tyr Gly Gln Leu Phe Asn Val Trp Phe Cys Phe Ala Val Thr Leu Thr Ile Phe  
 TCG ACC ACA TTC ACA AAC TGT TAT GGG CAA CTC TTC AAT GTT TGG TTC TGC TTT GCC GTT ACT CTC ACA ATC TTC 260 270  
 825  
 Pro Val Met Met Thr Val Thr Thr Arg Gly Asp Ser Ser Gly Phe Leu Asn Lys Ile Met Ser Glu Asn Asp Glu Ile  
 CCT GTT ATG ATG ACC GTT ACC ACT CGT GGA GAT TCC GGC TTC CTA AAC AAA ATT ATG TCT TCT GAA AAC GAT GAA ATC 280 290 300  
 900  
 Tyr Thr Leu Leu Thr Ser Phe Leu Val Phe Asn Leu Phe Ala Ala Ile Gly Ser Ile Val Ala Ser Lys Ile His  
 TAC ACT TTG CTC ACA AGT TTC CTC CTC TTC AAT TTG TTC GCT GCG ATT GGA TCC ATA GTT GCT TCC AAG ATT CAC 310 320  
 975  
 Trp Pro Thr Pro Arg Lys Tyr Leu Lys Phe Ala Ile Ile Leu Arg Ala Leu Phe Ile Phe Phe Phe Cys Asn  
 TCG CCG ACA CCC CGT TAC CTC AAA TTT GCC ATA ATC TTG CGT GCT CTT TTC ATT CCA TTC TTC TTC TGC AAC 330 340 350  
 1050  
 Tyr Arg Val Gln Thr Arg Ala Tyr Pro Val Phe Phe Glu Ser Thr Asp Ile Phe Val Ile Gly Gly Ile Ala Met  
 TAT CGT GTC CAG ACG CGT GCT TAT CCT GTT TTC TTT GAG TCT ACT GAC ATT TTT GTG ATT GGT GGA ATT GCC ATG 360 370  
 1125  
 Ser Phe Ser His Gly Tyr Leu Ser Ala Leu Ala Met Gly Tyr Thr Pro Asn Val Val Pro Ser His Tyr Ser Arg  
 TCT TTT TCA CAT GGA TAC CTC AGC GCT CTG GCA ATG GGA TAC ACT CCA AAC GTC GTC CCA TCT CAC TAC TCA ACA 380 390 400  
 1200  
 Phe Ala Ala Gln Leu Ser Val Cys Thr Leu Met Val Gly Leu Leu Thr Gly Gly Leu Trp Pro Val Val Ile Glu  
 TTT GCC GCT CAG CTT TCC GTT TGC ACT CTT ATG GTT GGC CTT CTC ACC GGT GGC CTG TGC CCC GTT GTT ATT GAG 410 420  
 1275  
 His Phe Val Asp Lys Pro Ser Ile Leu TAA ATATTATAGCATTAAGATACTTGTATATGTTCTTTTATTAAGCTGTGCAATAAA 430 434 (SEQ ID NO: 63)  
 CAC TTC GTG GAC AAG CCA AGT ATC TTA TAA ATATTATAGCATTAAGATACTTGTATATGTTCTTTTATTAAGCTGTGCAATAAA  
 ATAAATTAATTAATAAAAAAAAAAAAA 1388 (SEQ ID NO: 36)

FIG. 9B

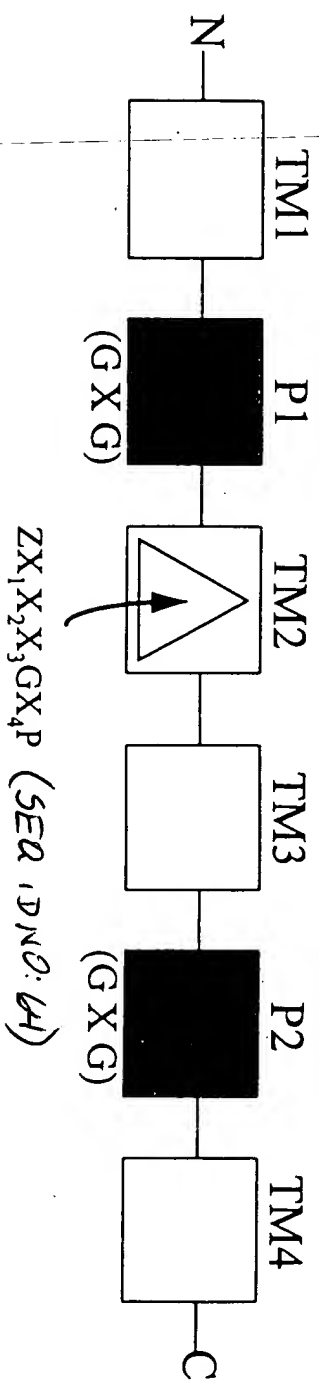


FIG. 10